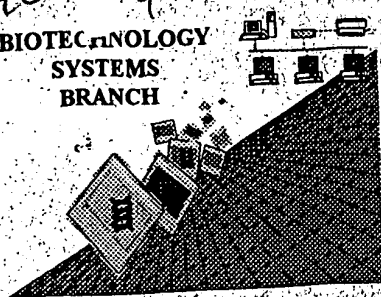


0400-ny-10-01-0280

BIOTECHNOLOGY
SYSTEMS
BRANCH



RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/805,467
Source: OIPE
Date Processed by STIC: 3/27/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).

Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

OIFE

RAW SEQUENCE LISTING DATE: 03/27/2001
 PATENT APPLICATION: US/09/805,467 TIME: 09:15:09

Input Set : A:\4974.00453 sequence listing.txt
 Output Set: N:\CRF3\03272001\I805467.raw

Does Not Comply
 Corrected Diskette Needed

5 <110> APPLICANT: APPLICANT: Ramakrishnan, Shyam
 7 <120> TITLE OF INVENTION: TITLE: Regulation of Human Lipoxin A4
 8 Receptor-Like Protein
 10 <130> FILE REFERENCE: DOCKET/FILE REFERENCE: 4974.00453
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/09/805,467
 C--> 12 <141> CURRENT FILING DATE: 2001-03-14
 12 <150> PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: 60/189,037
 W--> 13 <151> PRIOR FILING DATE: FILING DATE: 2000-03-14
 15 <150> PRIOR APPLICATION NUMBER: PRIOR APPLICATION NUMBER: PCT application (attorney docket LIO-005)
 W--> 16 <151> PRIOR FILING DATE: FILING DATE: 2000-03-12
 E--> 19 <160> NUMBER OF SEQ ID NOS: NUMBER OF SEQUENCES: 5
 21 <170> SOFTWARE: SOFTWARE: FastSEQ for Windows Version 4.0

ERRORRED SEQUENCES

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 24 <211> LENGTH: LENGTH: 1413
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 55 <211> LENGTH: LENGTH: 470

see
 next
 page
 for explanation

09/805,467 2

~~SEQUENCE LISTING~~

<110> ~~APPLICANT:~~ Ramakrishnan, Shyam
<120> ~~TITLE:~~ Regulation of Human Lipoxin A4
Receptor-Like Protein
<130> ~~DOCKET/FILE REFERENCE:~~ 4974.00453
<150> ~~PRIOR APPLICATION NUMBER:~~ 60/189,037
<151> ~~FILING DATE:~~ 2000-03-14

<150> ~~PRIOR APPLICATION NUMBER:~~ PCT application (attorney docket LIO-005)
<151> ~~FILING DATE:~~ 2000-03-12

<160> ~~NUMBER OF SEQUENCES:~~ 5
<170> ~~SOFTWARE:~~ FastSEQ for Windows Version 4.0

<210> ~~SEQ ID NO:~~ 1
<211> ~~LENGTH:~~ 1413
<212> ~~TYPE:~~ DNA
<213> ~~ORGANISM:~~ Homo sapiens

<400> ~~SEQ ID NO:~~ 1
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sample of submitted file

Do NOT insert alphabetical headings, when using new
format. Just use numeric identifiers.

FYI

Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.